particles(blanklv group), respectively, as the over-expression group and blank group. Instantaneous intervention VAF by *ifi*204 small interfering (ifi204siRNA group) or blank small interfering RNA (Control SiRNA group) ,as ifi204siRNA group and control SiRNA group. VAF was untreated as a negative group. Cell apoptosis was detected by flow cytometry; cell migration by cell scratch and transwell; the mRNA and protein expression of p204/p53/P21 were detected by Real-Time PCR and Western blot.

RESULTS Compared with those in the blank lv group ,controls iRNA group ,ifi204siRNA group or Negative group, in ifi204lv group ,P204/P53/P21 mRNA and protein expression increased, rate of apoptosis significantly increased ($P<0.05$), and cell migration speed reduced ($P<0.05$). Transfection of ifi204siRNA inhibit P204 /P53/P21 mRNA and protein expression ($P<0.05$), improves cell viability($P<0.05$), inhibits cell apoptosis($P<0.05$), accelerates the speed of cell migration($P<0.05$).

CONCLUSIONS P204 based expression in VAF. Effects of *ifi204* gene expression on apoptosis and migration of rat vascular adventitial fibroblast may be related to activation of p53 and P21.

GW26-e4501

Expression of Notch Signaling Molecules in the Process of microRNA-1 Inducing Rat Bone Marrow Mesenchymal Stem Cells Into Cardiomyocyte-Like Cells

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OBJECTIVES To investigate the effect of miR-1 on MSCs differentiation into cardiac phenotypes and the expression changes of Notch signaling molecules in this process.

METHODS MSCs were isolated from rat bone marrow by the whole bone marrow adherence method; MSCs identified by flow cytometry were introduced by the lentiviral vectors expressing miR-1 (MSCsmiR-1), Which were then divided into four groups: control group, 4-day culture group, 6-day culture group,15-day culture group; The cell morphology was examined by light microscope, miR-1 and cardiomyocyte-specific genes including GATA-4, cTnI and α-actin were examined by real-time quantitative polymerase chain reaction (qPCR),and the expression of cTnI and α-actin was detected by immunofluorescence and Western blot respectively; Meanwhile, $MSCs^{miR-1}$ cells were detected for the expression of genes related to notch signaling pathway by qPCR.

RESULTS Isolated MSCs displayed a stable spindle-phenotype and showed characteristic swirling growth. More than 98% of the MSCs population expressed CD44 and CD29 for MSCs phenotype; Meanwhile, less than 1% cells were CD45 positive. Compared with control cells, $MSCs^{miR-1}$ highly expressed miR-1 and showed a higher expression of cardiomyocyte-specific genes, including GATA-4, cTnI and α-actin, cTnI was detected by immunofluorescence in $MSCs^{miR-1}$ after miR-1 transduction for 4 days, and gradually increased afterwards. Western blot further confirmed the expression of α-actin in $MSCs^{miR-1}$. The mRNA expression of Jagged1, Notch1, Notch3 and Hey2 reduced significantly in $MSCs^{miR-1}$ during its differentiation into cardiomyocyte-like cells, and reached the minimum on day 15.

CONCLUSIONS Our study suggests that transduction of miR-1 into rat MSCs induce cell differentiation into cardiomyocyte-like cells, which is in company with down-regulation mRNA expression of Jagged1-Notch1/ Notch3-Hey2 in the Notch pathway.

GW26-e4653

Adiponectin Promoter Gene Polymorphisms Are Associated With the Protection of Coronary Atherosclerosis

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OBJECTIVES Genetic researches have indicated that polymorphic mutation in promoter region of adiponectin gene might influence its promoter transcriptional activity, which, as many researches demonstrate, leads to decrease in serum adiponectin levels. However, it remains uncertain whether it is associated with the risk of coronary atherosclerosis. In the present study, we aimed to determine the association between single nucleotide polymorphisms of adiponectin promoter region and coronary atherosclerosis in early-onset coronary artery disease (EOCAD) population.

METHODS According to age (male ≤55, female ≤65), ECG and coronary angiography results, EOCAD group (382 cases) and control group (305 cases) were enrolled into the present study. Detailed archives were set up for all the patients, including general information, demographics, personal history, family history, medication history, and biochemical indicators. After genomic DNA was extracted with Hipure Blood DNA Kits, three loci rs16861194 (-11426A/G), rs17300539 (-11391G/A) and rs266729 (-11377C/G) in the promoter region of adiponectin gene were sequenced and genotyped.

RESULTS There were no significant differences of genotype and allele frequencies in -11426 A/G locus between control and EOCAD group ($P>0.05$). All the genotypes in -11391G/A locus were wild type, while mutant and heterozygous type were failed to detect in this study population. In the -11377 locus, genotype GG, CG and allele G of EOCAD group were significantly higher than those of control group (all $P<0.05$). Genotype GG was significantly associated with lower adiponectin levels, and could significantly increase the CAD risk (OR =1.361; 95%CI, 1.114-1.621; $P=0.032$). Haplotype AGG was independently associated with CAD risk (OR =1.646; 95%CI, 1.027-2.637; $P=0.038$).

CONCLUSIONS Mutation in -11377C/G locus of adiponectin promoter region was negatively associated with lower adiponectin levels, and could increase the risk of CAD. Haplotype AGG was an independently risk factor for coronary atherosclerosis.

GW26-e4725

MicroRNA-21 Regulates Post-Ischemic Inflammation Triggered by DAMPs in Myocardial Infarction Through Targeting STK40

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OBJECTIVES Post-ischemic inflammation is an essential step in the progression of myocardial infarction (MI). Damage-associated molecular patterns (DAMPs) are implicated in the activation of infiltrating immune cells and triggering release of inflammatory cytokines. MicroRNA-21 (miR-21) has been shown to inhibit apoptosis of cardiomyocytes and promote cardiac fibrosis. However, the role of miR-21 in post-ischemic inflammation remains obscure. Our aim is to determine whether miR-21 regulates DAMPs-triggered inflammation after MI in mice and investigate the underlying signal mechanism.

METHODS We constructed the GFP adenovirus vector expressing miR-21 (GFP-Ad-miR-21) and control adenovirus vector (GFP-Ad). For in vivo experiment, myocardial infarction of mice was induced by left coronary ligation and then the GFP-Ad-miR-21 or GFP-Ad was directly injected into the remote region of infarct heart. Mice were divided into four groups: MI-Ad-miR-21, MI-Ad, sham-Ad-miR-21, sham-Ad. The LVEF, LVFS, LVESD and LVEDD were detected by echocardiography 60 days after MI induction and the myocardial infarct size was analyzed by TTC staining. The inflammatory cytokines were evaluated by Q-PCR, ELISA and IHC. Meanwhile, DAMPs-induced inflammatory response of macrophage was imitated with stimulation of recombinant mouse HSP60 (rmHSP60) or recombinant mouse HMGB1 (rmHMGB1) after transfection with miR-21 mimics. The expressions of inflammatory cytokines and the activation of MAPK and NF-κB signal in macrophage were determined, respectively. In mechanism, we analyzed the targeting gene using TargetScan 6.2 and verify the interaction between miR-21 and targeting gene with luciferase reporter assay.

RESULTS In MI-Ad-miR-21, LVEF and LVFS were significantly decreased, and LVESD, LVEDD and myocardial infarct size were apparently increased. In heart tissue of MI-Ad-miR-21, the expression of IL-1β, IL-6, IL-12 and TNF-α in remote region were higher than that in MI-Ad. Overexpression of miR-21 mimics notably increased the production of IL-1β, IL-6, IL-12 and TNF-α in mouse macrophages stimulated with rmHSP60 or rmHMGB1. Moreover, the phosphorylated levels of ERK, JNK, p38 and IKK-α/β were significantly increased when overexpression of miR-21 mimics in the rmHSP60 or rmHmGB1-stimulatedmacrophages. Furthermore, we found that miR-21 mimic markedly decreased the luciferase activity of wild type STK40 luciferase (STK40-Luc). Consistently, miR-21 inhibitor increased the luciferase activity of wild type STK40-Luc. In addition, the expression of STK40 was found to be reduced after transfection with miR-21 mimics in macrophage.

CONCLUSIONS These data show that miR-21 up-regulates inflammatory response after MI by enhancing the activation of MAPK and NF-κB signaling pathway. MiR-21 inhibits the protein and mRNA expression levels of the STK40 in mouse macrophages, together with previous study that STK40 is the negative regulator of MAPK and NF-κB pathway, these data indicate that miR-21 promote MI-induced inflammatory response by regulating the target gene STK40.